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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2009; month=4; day=30; hr=16; min=6; sec=22; ms=992;]

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Application No: 10512004

Version No: 2.0

Input Set:

Output Set:

Started: 2009-04-23 13:03:04.945

Finished: 2009-04-23 13:03:05.935

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 990 ms

Total Warnings: 14

Total Errors: 0

No. of SeqIDs Defined: 19

Actual SeqID Count: 19

Error code	Error Description
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SEQUENCE LISTING

<110> Hellenic Pasteur Institute
 Association Francaise Contre Les Myopathies
 Tzartos, Socrates
 Mamalaki, Avgi

<120> Production of recombinant fragments of muscle acetylcholine
 receptor and their use for ex vivo immunoadsorption of anti-Ch
 receptor antibodies from myasthenic patients

<130> P023389US

<140> 10512004

<141> 2009-04-23

<150> GR 20020100190

<151> 2002-04-17

<160> 19

<170> PatentIn version 3.5

<210> 1

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<212> PRT

<213> Pichia pastoris

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<222> (143)..(143)

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Tyr	Ser	Ser	Val	Val	Arg	Pro	Val	Glu	Asp	His	Arg	Gln	Val	Val	Glu
			20					25					30		

Val	Thr	Val	Gly	Leu	Gln	Leu	Ile	Gln	Leu	Ile	Asn	Val	Asp	Glu	Val
		35					40					45			

Asn	Gln	Ile	Val	Thr	Thr	Asn	Val	Arg	Leu	Lys	Gln	Gln	Trp	Val	Asp
50						55					60				

Tyr	Asn	Leu	Lys	Trp	Asn	Pro	Asp	Asp	Tyr	Gly	Gly	Val	Lys	Lys	Ile
65					70					75					80

His	Ile	Pro	Ser	Glu	Lys	Ile	Trp	Arg	Pro	Asp	Leu	Val	Leu	Tyr	Asn
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85

90

95

Asn Ala Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val Leu Leu
 100 105 110

Gln Tyr Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe Lys Ser
 115 120 125

Tyr Cys Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln Asn Cys
 130 135 140

Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val Ala Ile
 145 150 155 160

Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu Ser Gly
 165 170 175

Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val Thr Tyr
 180 185 190

Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His Phe Val
 195 200 205

Met Gln Arg Leu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser
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Ala Val Asp His His His His His His
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20 25 30

Pro Asn Leu Arg Pro Ala Glu Arg Asp Ser Asp Val Val Asn Val Ser
35 40 45

Leu Lys Leu Thr Leu Thr Asn Leu Ile Ser Leu Asn Glu Arg Glu Glu
50 55 60

Ala Leu Thr Thr Asn Val Trp Ile Glu Met Gln Trp Cys Asp Tyr Arg
65 70 75 80

Leu Arg Trp Asp Pro Arg Asp Tyr Glu Gly Leu Trp Val Leu Arg Val
85 90 95

Pro Ser Thr Met Val Trp Arg Pro Asp Ile Val Leu Glu Asn Asn Val
100 105 110

Asp Gly Val Phe Glu Val Ala Leu Tyr Cys Asn Val Leu Val Ser Pro
115 120 125

Asp Gly Cys Ile Tyr Trp Leu Pro Pro Ala Ile Phe Arg Ser Ala Cys
130 135 140

Ser Ile Ser Val Thr Tyr Phe Pro Phe Asp Trp Gln Asn Cys Ser Leu
145 150 155 160

Ile Phe Gln Ser Gln Thr Tyr Ser Thr Asn Glu Ile Asp Leu Gln Leu
165 170 175

Ser Gln Glu Asp Gly Gln Thr Ile Glu Trp Ile Phe Ile Asp Pro Glu
180 185 190

Ala Phe Thr Glu Asn Gly Glu Trp Ala Ile Gln His Arg Pro Ala Lys
195 200 205

Met Leu Leu Asp Pro Ala Ala Pro Ala Gln Glu Ala Gly His Gln Lys
210 215 220

Val Val Phe Tyr Leu Leu Ile Gln Arg Lys His His His His His His
225 230 235 240

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<222> (82)..(82)

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20 25 30

Pro Gly Ser Arg Pro Val Arg Glu Pro Glu Asp Thr Val Thr Ile Ser
35 40 45

Leu Lys Val Thr Leu Thr Asn Leu Ile Ser Leu Asn Glu Lys Glu Glu
50 55 60

Thr Leu Thr Thr Ser Val Trp Ile Gly Ile Asp Trp Gln Asp Tyr Arg
65 70 75 80

Leu Asn Tyr Ser Lys Asp Asp Phe Gly Gly Ile Glu Thr Leu Arg Val
85 90 95

Pro Ser Glu Leu Val Trp Leu Pro Glu Ile Val Leu Glu Asn Asn Ile
100 105 110

Asp Gly Gln Phe Gly Val Ala Tyr Asp Ala Asn Val Leu Val Tyr Glu
115 120 125

Gly Gly Ser Val Thr Trp Leu Pro Pro Ala Ile Tyr Arg Ser Val Cys
130 135 140

Ala Val Glu Val Thr Tyr Phe Pro Phe Asp Trp Gln Asn Cys Ser Leu
145 150 155 160

Ile Phe Arg Ser Gln Thr Tyr Asn Ala Glu Glu Val Glu Phe Thr Phe
165 170 175

Ala Val Asp Asn Asp Gly Lys Thr Ile Asn Lys Ile Asp Ile Asp Thr
180 185 190

Glu Ala Tyr Thr Glu Asn Gly Glu Trp Ala Ile Asp Phe Cys Pro Gly
195 200 205

Val Ile Arg Arg His His Gly Gly Ala Thr Asp Gly Pro Gly Glu Thr
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Asp Val Ile Tyr Ser Leu Ile Ile Arg Arg Lys His His His His His
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His

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Leu Asn Glu Glu Glu Arg Leu Ile Arg His Leu Phe Gln Glu Lys Gly
20 25 30

Tyr Asn Lys Glu Leu Arg Pro Val Ala His Lys Glu Glu Ser Val Asp
35 40 45

Val Ala Leu Ala Leu Thr Leu Ser Asn Leu Ile Ser Leu Lys Glu Val

50

55

60

Glu Glu Thr Leu Thr Thr Asn Val Trp Ile Glu His Gly Trp Thr Asp
 65 70 75 80

Asn Arg Leu Lys Trp Asn Ala Glu Glu Phe Gly Asn Ile Ser Val Leu
 85 90 95

Arg Leu Pro Pro Asp Met Val Trp Leu Pro Glu Ile Val Leu Glu Asn
 100 105 110

Asn Asn Asp Gly Ser Phe Gln Ile Ser Tyr Ser Cys Asn Val Leu Val
 115 120 125

Tyr His Tyr Gly Phe Val Tyr Trp Leu Pro Pro Ala Ile Phe Arg Ser
 130 135 140

Ser Cys Pro Ile Ser Val Thr Tyr Phe Pro Phe Asp Trp Gln Asn Cys
 145 150 155 160

Ser Leu Lys Phe Ser Ser Leu Lys Tyr Thr Ala Lys Glu Ile Thr Leu
 165 170 175

Ser Leu Lys Gln Asp Ala Lys Glu Asn Arg Thr Tyr Pro Val Glu Trp
 180 185 190

Ile Ile Ile Asp Pro Glu Gly Phe Thr Glu Asn Gly Glu Trp Glu Ile
 195 200 205

Val His Arg Pro Ala Arg Val Asn Val Asp Pro Arg Ala Pro Leu Asp
 210 215 220

Ser Pro Ser Arg Gln Asp Ile Thr Phe Tyr Leu Ile Ile Arg Arg Lys
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Glu Ala Glu Ala Tyr Val Asp Tyr Lys Asp Asp Asp Asp Lys Glu Phe
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Ser Glu Ala Glu Gly Arg Leu Arg Glu Lys Leu Phe Ser Gly Tyr Asp
20 25 30

Ser Ser Val Arg Pro Ala Arg Glu Val Gly Asp Arg Val Arg Val Ser
35 40 45

Val Gly Leu Ile Leu Ala Gln Leu Ile Ser Leu Asn Glu Lys Asp Glu
50 55 60

Glu Met Ser Thr Lys Val Tyr Leu Asp Leu Glu Trp Thr Asp Tyr Arg
65 70 75 80

Leu Ser Trp Asp Pro Ala Glu His Asp Gly Ile Asp Ser Leu Arg Ile
85 90 95

Thr Ala Glu Ser Val Trp Leu Pro Asp Val Val Leu Leu Asn Asn Asn
100 105 110

Asp Gly Asn Phe Asp Val Ala Leu Asp Ile Ser Val Val Val Ser Ser
115 120 125

Asp Gly Ser Val Arg Trp Gln Pro Pro Gly Ile Tyr Arg Ser Ser Cys
130 135 140

Ser Ile Gln Val Thr Tyr Phe Pro Phe Asp Trp Gln Asn Cys Thr Met
145 150 155 160

Val Phe Ser Ser Tyr Ser Tyr Asp Ser Ser Glu Val Ser Leu Gln Thr
165 170 175

Gly Leu Gly Pro Asp Gly Gln Gly His Gln Glu Ile His Ile His Glu
180 185 190

Gly Thr Phe Ile Glu Asn Gly Gln Trp Glu Asn Ile His Lys Pro Ser
195 200 205

Arg Leu Ile Gln Pro Pro Gly Asp Pro Arg Gly Gly Arg Glu Gly Gln
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Arg Gln Glu Val Ile Phe Tyr Leu Ile Ile Arg Arg Lys His His His
225 230 235 240

His His His

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Asp Tyr Lys Asp Asp Asp Asp Lys
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<210> 15

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gtagattaca aggatgacga tgacaaag 28

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<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 16

gtgtggcagc gaattcctga acgag 25

<210> 17

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 17

gatgtagaat tctcacttgc ggcgg 25

<210> 18

<211> 79

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 18

gcggcgcgat gaaggttctg tgggctgcgt tgctggtcac attcctggca ggatgccagg 60

cctccgaaca tgagaccg 79

<210> 19

<211> 40

<212> DNA

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<220>

<223> Primer

<400> 19

ccgagcctcg agtcaatgat gatgatgatg atggtcgacg

40